

COMPUTER METHOD AND APPARATUS FOR UNIFORM
REPRESENTATION OF GENOME SEQUENCES

ABSTRACT OF THE DISCLOSURE

A method and apparatus transforms typically differing length text string representations (i.e., sequences) of biological fragments into uniform length representations. A comparison database stores a predefined number of known biological sequences. A comparison routine compares and scores a subject sequence against each known sequence in the database. Each individual score (one for each known sequence in the database) serves as a vector element forming a fixed length vector representation of the subject sequence. Vector length equals the predefined number of known biological sequences in the database. Scoring is a probability or an occurrence count of the known biological sequence in the subject sequence.

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